Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims:

1-21. (cancelled)

22. (previously presented) An isolated oligonucleotide sequence comprising a response element that binds to a nuclear receptor of the Nur family of nuclear receptors, said response element comprising nucleotide sequence X_8 L_6 Y_8, wherein:

a) X_8 and Y_8 are two half site sequences of 8 nucleotides which are configured as an everted repeat;

b) L_6 separates said half site sequences, with L being 6 nucleotides and being independently selected from A,T,C,or G;

c) X_8 having nucleotide sequence N_6TT, and Y_8 having nucleotide sequence AAN_6, wherein N is selected from A,T,C,or G, such that said sequence of X_8 and Y_8 share homology with the NBRE sequence defined by the hexanucleotide sequence AGGTCA (SEQ ID NO: 3), and its complement TGACCT (SEQ ID NO: 29), respectively, and wherein said response element is capable of binding to a dimer consisting of two partners which are selected from members of the Nur family of nuclear receptors.

23. (previously presented) The oligonucleotide sequence of claim 22, wherein 4 out of 6 nucleotides of N_6 are identical to said AGGTCA (SEQ ID NO: 3) or TGACCT (SEQ ID NO: 29) sequences.

24. (previously presented) The oligonucleotide sequence of claim 23, wherein AAN_6 has a sequence selected from the group consisting of AAATATCA (SEQ ID NO:7), AAATGCCA (SEQ ID NO:8), AAAGGTCA (SEQ ID NO:1), and functional derivatives thereof.

25. (previously presented) The oligonucleotide sequence of claim 23, wherein N_6TT has a sequence selected from the group consisting of TGATATTT (SEQ ID NO: 30), TGGCATTT (SEQ ID NO: 31), TGACCTTT (SEQ ID NO: 32), and functional derivatives thereof.

26. (previously presented) The oligonucleotide sequence of claim 25, wherein said response element comprises a nucleotide sequence selected from the group consisting of :

GTGATATTTXXXXXXAAATGCCAG (SEQ ID NO:9),
TGATATTTXXXXXXAAATGCCA (SEQ ID NO:10),
GTGATATTTXXXXXXAAATATCAC (SEQ ID NO:11),
TGATATTTXXXXXXAAATATCA (SEQ ID NO:12),
CTGGCATTTXXXXXXAAATGCCAG (SEQ ID NO:13),
TGGCATTTXXXXXXAAATGCCA (SEQ ID NO:14),
QTGACCTTTXXXXXXAAAGGTCAQ (SEQ ID NO:15),
TGACCTTTXXXXXXAAAGGTCA (SEQ ID NO:16),
QTGUYATTTXXXXXXAAATUYCAQ (SEQ ID NO:17),
TGUYATTTXXXXXXAAATUYCA (SEQ ID NO:18),
GTGATATTTACCTCCAAATGCCAG (SEQ ID NO:19),
TGATATTTACCTCCAAATGCCA (SEQ ID NO:20),
GTGATATTTACCTCCAAATATCAC (SEQ ID NO:21),
TGATATTTACCTCCAAATATCA (SEQ ID NO:22),
CTGGCATTTACCTCCAAATGCCAG (SEQ ID NO:23),
TGGCATTTACCTCCAAATGCCA (SEQ ID NO:24),
QTGACCTTTACCTCCAAAGGTCAQ (SEQ ID NO:25),
TGACCTTTACCTCCAAAGGTCA (SEQ ID NO:26),
QTGUYATTTACCTCCAAATUYCAQ (SEQ ID NO:27),
TGUYATTTACCTCCAAATUYCA (SEQ ID NO:28),

complements and functional derivatives thereof, wherein X is independently selected from A,T,C,or G, U is a purine, Y is a pyrimidine, and Q is C or G.

27. (previously presented) The oligonucleotide sequence of claim 26, wherein said response element comprises a nucleic acid sequence selected from the group consisting of: GTGATATTTXXXXXXAAATGCCAG (SEQ ID NO:9) and TGACCTTTXXXXXXAAAGGTCA (SEQ ID NO:16).

28. (previously presented) The oligonucleotide sequence of claim 26, wherein said response element comprises nucleic acid sequence TGATATTTACCTCCAAATGCCA (SEQ ID NO:20).

29. (previously presented) The oligonucleotide sequence of claim 27, wherein said response element comprises nucleic acid sequence GTGATATTTACCTCCAAATGCCAG (SEQ ID NO:19).

30. (previously presented) The oligonucleotide sequence of claim 27, wherein said response element comprises nucleic acid sequence TGACCTTTXXXXXXAAAGGTCA (SEQ ID NO:16).

31. (previously presented) The oligonucleotide sequence of claim 22, wherein said member of the Nur family of nuclear receptors is selected from the group consisting of: Nur77, NGFI-B, N10, NAK1, TR3, Nurr-1, RNR-1, NOT, TINUR, NOR-1 and MINOR.

32. (previously presented) The oligonucleotide sequence of claim 22, wherein said response element binds to a dimer formed between a first and second member of said Nur family of nuclear receptors, and wherein said first and second members are the same member of the Nur family of nuclear receptors, thereby forming a homodimer.

33. (previously presented) The oligonucleotide sequence of claim 22, wherein said response element binds to a dimer formed between a first and second member of said Nur family of nuclear receptors, and wherein said first and second members are different members of the Nur family of nuclear receptors, thereby forming a heterodimer.

34. (previously presented) A DNA construct comprising the oligonucleotide sequence of claim 22, operably linked to a promoter, which promoter is operably linked to a heterologous gene, wherein the DNA construct is linked in such a manner that the gene is under the transcriptional control of the oligonucleotide sequence and promoter.

35. (previously presented) The DNA construct of claim 34, wherein said oligonucleotide sequence comprises a multimer of at least one of said response element.

36. (previously presented) The DNA construct of claim 34, wherein the heterologous gene is a reporter gene.

37. (previously presented) A host cell transfected with the DNA construct of claim 34.

38. (previously presented) A method for controlled expression of a heterologous gene of interest comprising culturing a host cell according to claim 37 in the presence of an appropriate regulatory protein.

39. (previously presented) The method according to claim 38, wherein the regulatory protein comprises a member of the Nur family of nuclear receptors.

40. (currently amended) A method for detecting a modulator of transcription at a Nur response element (Nur-RE), wherein said Nur-RE is an oligonucleotide sequence comprising a response element that binds to a nuclear receptor of the Nur family of nuclear receptors, said response element comprising nucleotide sequence X_8 L_6 Y_8, wherein:

a) X_8 and Y_8 are two half site sequences of 8 nucleotides which are configured as an everted repeat;

b) L_6 separates said half site sequences, with L being 6 nucleotides and being independently selected from A,T,C,or G;

c) X_8 having nucleotide sequence N_6TT, and Y_8 having nucleotide sequence AAN_6, wherein N is selected from A,T,C,or G, such that said sequence of X_8 and Y_8 share homology with the NBRE sequence defined by ~~nucleotide~~ the hexanucleotide sequence AGGTCA (SEQ ID NO: 3), and its complement TGACCT (SEQ ID NO: 29), respectively, and wherein said response element is capable of binding to a dimer consisting of two partners which are selected from members of the Nur family of nuclear receptors,

comprising contacting a sample with said host cell according to claim 37, and comparing the level of expression of said reporter gene in the presence of the sample and in the absence thereof.

41. (currently amended) A method for measuring the ability of a compound to modulate transcription at a Nur response element (Nur-RE), wherein said Nur-RE is an oligonucleotide sequence comprising a response element that binds to a nuclear receptor of the Nur family of nuclear receptors, said response element comprising nucleotide sequence X_8 L_6 Y_8, wherein:

a) X_8 and Y_8 are two half site sequences of 8 nucleotides which are configured as an everted repeat;

b) L_6 separates said half site sequences, with L being 6 nucleotides and being independently selected from A,T, C, or G;

c) X_8 having nucleotide sequence N_6TT, and Y_8 having nucleotide sequence AAN_6, wherein N is selected from A,T, C, or G, such that said sequence of X_8 and Y_8 share homology with the NBRE sequence defined by ~~nucleotide~~ the hexanucleotide sequence AGGTCA (SEQ ID NO:3), and its complement TGACCT (SEQ ID NO: 29), respectively, and wherein said response element is capable of binding to a dimer consisting of two partners which are selected from members of the Nur family of nuclear receptors,

comprising:

~~a)~~ i) contacting said compound with said host cell of claim 37, under conditions conducive to the expression of said heterologous gene in response to said compound; and

~~b)~~ ii) comparing the level of gene expression in step ~~a)~~ i) with the level of gene expression from said host cell in the absence of said compound.

42. (previously presented) The method of claim 41 whereby a ligand which is selective for Nur family transcriptional complexes is identified.

43-47 (withdrawn)